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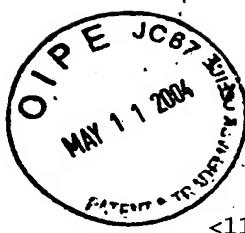
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279152RX  
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Phe Gln Lys Leu Ser Glu Pro Leu Asn His Ser Tyr Gln Ala Ile Ile  
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165 170 175

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Leu Thr Ala Thr Leu Leu Ile Leu Ser Leu Lys Arg His Thr Leu His  
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Met Gly Ser Asn Ala Thr Gly Ser Asn Asp Pro Ser Met Glu Ala His  
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Met Gly Ala Ile Lys Ala Ile Ser Tyr Phe Leu Ile Leu Tyr Ile Phe  
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Asn Ala Val Ala Leu Phe Ile Tyr Leu Ser Asn Met Phe Asp Ile Asn  
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Arg Gly Lys Thr Leu Pro Thr Gly Asp Arg Ile Met Leu Met Leu Ser  
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Phe Lys Val Ile Thr Val Phe Leu Asn His Ser Asn Leu Trp Phe Ala  
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Ala Trp Leu Lys Val Phe Tyr Cys Leu Arg Ile Ala Asn Phe Asn His  
115 120 125

Pro Leu Phe Phe Leu Met Lys Arg Lys Ile Ile Val Leu Met Pro Trp  
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Ser Arg Asp Val Phe Asn Val Tyr Val Asn Ser Ser Ile Pro Ile Pro  
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Asn Leu Val Phe Phe Tyr Asn Met Gly Ile Phe Val Pro Leu Ile Met  
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210 215 220

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Val Leu Val Ile Val Leu Gly Ser Leu Phe Phe Leu Val Cys His Leu  
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265

270

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&lt;210&gt; 14

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 14

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Phe Val Leu Gly Asn Val Ala Asn Gly Phe Ile Ala Leu Val Asn Val  
20 25 30

Ile Asp Trp Val Asn Thr Arg Lys Ile Ser Ser Ala Glu Gln Ile Leu  
35 40 45

Thr Ala Leu Val Val Ser Arg Ile Gly Leu Leu Trp Val Met Leu Phe  
50 55 60

Leu Trp Tyr Ala Thr Val Phe Asn Ser Ala Leu Tyr Gly Leu Glu Val  
65 70 75 80

Arg Ile Val Ala Ser Asn Ala Trp Ala Val Thr Asn His Phe Ser Met  
85 90 95

Trp Leu Ala Ala Ser Leu Ser Ile Phe Cys Leu Leu Lys Ile Ala Asn  
100 105 110

Phe Ser Asn Leu Ile Ser Leu His Leu Lys Lys Arg Ile Lys Ser Val  
Page 10

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115

120

125

Val Leu Val Ile Leu Leu Gly Pro Leu Val Phe Leu Ile Cys Asn Leu  
130 135 140

Ala Val Ile Thr Met Asp Glu Arg Val Trp Thr Lys Glu Tyr Glu Gly  
145 150 155 160

Asn Val Thr Trp Lys Ile Lys Leu Arg Asn Ala Ile His Leu Ser Ser  
165 170 175

Leu Thr Val Thr Thr Leu Ala Asn Leu Ile Pro Phe Thr Leu Ser Leu  
180 185 190

Ile Cys Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys  
195 200 205

Met Arg Leu His Ser Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His  
210 215 220

Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Met Leu Phe Ala Ile  
225 230 235 240

Tyr Phe Leu Cys Ile Ile Thr Ser Thr Trp Asn Leu Arg Thr Gln Gln  
245 250 255

Ser Lys Leu Val Leu Leu Leu Cys Gln Thr Val Ala Ile Met Tyr Pro  
260 265 270

Ser Phe His Ser Phe Ile Leu Ile Met Gly Ser Arg Lys Leu Lys Gln  
275 280 285

Thr Phe Leu Ser Val Leu Trp Gln Met Thr Arg  
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<210> 15

<211> 900

<212> DNA

<213> Homo sapiens

<400> 15

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<210> 16

<211> 299

<212> PRT

<213> Homo sapiens

<400> 16  
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 20 25 30  
 Ile Asp Trp Val Lys Arg Lys Lys Ile Ser Ser Ala Asp Gln Ile Leu  
 35 40 45  
 Thr Ala Leu Ala Val Ser Arg Ile Gly Leu Leu Trp Ala Leu Leu Leu  
 50 55 60  
 Asn Trp Tyr Leu Thr Val Leu Asn Pro Ala Phe Tyr Ser Val Glu Leu  
 65 70 75 80  
 Arg Ile Thr Ser Tyr Asn Ala Trp Val Val Thr Asn His Phe Ser Met  
 85 90 95  
 Trp Leu Ala Ala Asn Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn  
 100 105 110  
 Phe Ser Asn Leu Leu Phe Leu His Leu Lys Arg Arg Val Arg Ser Val  
 115 120 125  
 Ile Leu Val Ile Leu Leu Gly Thr Leu Ile Phe Leu Val Cys His Leu  
 130 135 140  
 Leu Val Ala Asn Met Asp Glu Ser Met Trp Ala Glu Glu Tyr Glu Gly  
 145 150 155 160  
 Asn Met Thr Gly Lys Met Lys Leu Arg Asn Thr Val His Leu Ser Tyr  
 165 170 175  
 Leu Thr Val Thr Thr Leu Trp Ser Phe Ile Pro Phe Thr Leu Ser Leu  
 180 185 190  
 Ile Ser Phe Leu Met Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys  
 195 200 205  
 Met Gln Leu His Gly Glu Gly Ser Gln Asp Leu Ser Thr Lys Val His  
 210 215 220  
 Ile Lys Ala Leu Gln Thr Leu Ile Ser Phe Leu Leu Cys Ala Ile  
 225 230 235 240  
 Phe Phe Leu Phe Leu Ile Val Ser Val Trp Ser Pro Arg Arg Leu Arg  
 245 250 255  
 Asn Asp Pro Val Val Met Val Ser Lys Ala Val Gly Asn Ile Tyr Leu  
 260 265 270  
 Ala Phe Asp Ser Phe Ile Leu Ile Trp Arg Thr Lys Lys Leu Lys His  
 275 280 285  
 Thr Phe Leu Leu Ile Leu Cys Gln Ile Arg Cys  
 290 295

<210> 17  
 <211> 924  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 17

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ttcatcctca	tcttcagca	cctcaagctt	cgaagcgtgt	tctcgcagct	cctgttgg	900	
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&lt;210&gt; 18

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 18

Met	Gln	Ala	Ala	Leu	Thr	Ala	Phe	Phe	Val	Leu	Leu	Phe	Ser	Leu	Leu
1				5					10					15	

Ser	Leu	Leu	Gly	Ile	Ala	Ala	Asn	Gly	Phe	Ile	Val	Leu	Val	Leu	Gly
			20					25					30		

Arg	Glu	Trp	Leu	Arg	Tyr	Gly	Arg	Leu	Leu	Pro	Leu	Asp	Met	Ile	Leu
	35						40					45			

Ile	Ser	Leu	Gly	Ala	Ser	Arg	Phe	Cys	Leu	Gln	Leu	Val	Gly	Thr	Val
	50					55					60				

His	Asn	Phe	Tyr	Tyr	Ser	Ala	Gln	Lys	Val	Glu	Tyr	Ser	Gly	Gly	Leu
	65				70				75				80		

Gly	Arg	Gln	Phe	Phe	His	Leu	His	Trp	His	Phe	Leu	Asn	Ser	Ala	Thr
	85					90				95					

Phe	Trp	Phe	Cys	Ser	Trp	Leu	Ser	Val	Leu	Phe	Cys	Val	Lys	Ile	Ala
	100					105						110			

Asn	Ile	Thr	His	Ser	Thr	Phe	Leu	Trp	Leu	Lys	Trp	Arg	Phe	Pro	Gly
	115					120					125				

Trp	Val	Pro	Trp	Leu	Leu	Leu	Gly	Ser	Val	Leu	Ile	Ser	Phe	Ile	Ile
	130				135					140					

Thr	Leu	Leu	Phe	Phe	Trp	Val	Asn	Tyr	Pro	Val	Tyr	Gln	Glu	Phe	Leu
	145					150				155			160		

Ile	Arg	Lys	Phe	Ser	Gly	Asn	Met	Thr	Tyr	Lys	Trp	Asn	Thr	Arg	Ile
	165						170					175			

Glu	Thr	Tyr	Tyr	Phe	Pro	Ser	Leu	Lys	Leu	Val	Ile	Trp	Ser	Ile	Pro
	180						185					190			

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Phe Ser Val Phe Leu Val Ser Ile Met Leu Leu Ile Asn Ser Leu Arg  
195 200 205

Arg His Thr Gln Arg Met Gln His Asn Gly His Ser Leu Gln Asp Pro  
210 215 220

Ser Thr Gln Ala His Thr Arg Ala Leu Lys Ser Leu Ile Ser Phe Leu  
225 230 235 240

Ile Leu Tyr Ala Leu Ser Phe Leu Ser Leu Ile Ile Asp Ala Ala Lys  
245 250 255

Phe Ile Ser Met Gln Asn Asp Phe Tyr Trp Pro Trp Gln Ile Ala Val  
260 265 270

Tyr Leu Cys Ile Ser Val His Pro Phe Ile Leu Ile Phe Ser Asn Leu  
275 280 285

Lys Leu Arg Ser Val Phe Ser Gln Leu Leu Leu Leu Ala Arg Gly Phe  
290 295 300

Trp Val Ala  
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<210> 19

<211> 930

<212> DNA

<213> Homo sapiens

<400> 19

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atctcttttgc ctgaccataat tctcaactgct ctggcagttct ccagagttgg tttactctgg 180  
gtatttagtat taaattggta tgcaactgag ttgaatccag ctttaacag tatagaagta 240  
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aacatgactt ggaagatcaa actgaggagt gcaatgttacc tttcaaaatac aacggttacc 540  
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<210> 20

<211> 309

<212> PRT

<213> Homo sapiens

<400> 20

Met Ile Thr Phe Leu Pro Ile Ile Phe Ser Ile Leu Ile Val Val Thr  
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20 25 30

Ile Glu Trp Phe Lys Arg Gln Lys Ile Ser Phe Ala Asp Gln Ile Leu  
35 40 45

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Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Val Leu  
50 55 60

Asn Trp Tyr Ala Thr Glu Leu Asn Pro Ala Phe Asn Ser Ile Glu Val  
65 70 75 80

Arg Ile Thr Ala Tyr Asn Val Trp Ala Val Ile Asn His Phe Ser Asn  
85 90 95

Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn  
100 105 110

Phe Ser Asn Leu Ile Phe Leu His Leu Lys Arg Arg Val Lys Ser Val  
115 120 125

Val Leu Val Ile Leu Leu Gly Pro Leu Leu Phe Leu Val Cys His Leu  
130 135 140

Phe Val Ile Asn Met Asn Gln Ile Ile Trp Thr Lys Glu Tyr Glu Gly  
145 150 155 160

Asn Met Thr Trp Lys Ile Lys Leu Arg Ser Ala Met Tyr Leu Ser Asn  
165 170 175

Thr Thr Val Thr Ile Leu Ala Asn Leu Val Pro Phe Thr Leu Thr Leu  
180 185 190

Ile Ser Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys  
195 200 205

Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Met Lys Val His  
210 215 220

Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Leu Leu Cys Ala Ile  
225 230 235 240

Tyr Phe Leu Ser Ile Ile Met Ser Val Trp Ser Phe Glu Ser Leu Glu  
245 250 255

Asn Lys Pro Val Phe Met Phe Cys Glu Ala Ile Ala Phe Ser Tyr Pro  
260 265 270

Ser Thr His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln  
275 280 285

Thr Phe Leu Ser Val Leu Trp His Val Arg Tyr Trp Val Lys Gly Glu  
290 295 300

Lys Pro Ser Ser Ser  
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<210> 21  
<211> 930  
<212> DNA  
<213> Homo sapiens

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<211> 885

<212> DNA

<213> Homo sapiens

<400> 22

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<211> 912

<212> DNA

<213> Mus sp.

<400> 23

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<210> 24

<211> 303

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Cys Tyr Asp Leu Phe Lys Ser Arg Thr Phe Leu Ile Leu Gln Thr Leu  
35 40 45  
Leu Met Cys Thr Gly Leu Ser Arg Leu Gly Leu Gln Ile Met Leu Met  
50 55 60  
Thr Gln Ser Phe Phe Ser Val Phe Phe Pro Tyr Ser Tyr Glu Glu Asn  
65 70 75 80  
Ile Tyr Ser Ser Asp Ile Met Phe Val Trp Met Phe Phe Ser Ser Ile  
85 90 95  
Gly Leu Trp Phe Ala Thr Cys Leu Ser Val Phe Tyr Cys Leu Lys Ile  
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Ser Gly Phe Thr Pro Pro Trp Phe Leu Trp Leu Lys Phe Arg Ile Ser  
115 120 125  
Lys Leu Ile Phe Trp Leu Leu Leu Gly Ser Leu Leu Ala Ser Leu Gly  
130 135 140  
Thr Ala Thr Val Cys Ile Glu Val Gly Phe Pro Leu Ile Glu Asp Gly  
145 150 155 160  
Tyr Val Leu Arg Asn Ala Gly Leu Asn Asp Ser Asn Ala Lys Leu Val  
165 170 175  
Arg Asn Asn Asp Leu Leu Leu Ile Asn Leu Ile Leu Leu Pro Leu  
180 185 190  
Ser Val Phe Val Met Cys Thr Ser Met Leu Phe Val Ser Leu Tyr Lys  
195 200 205  
His Met His Trp Met Gln Ser Glu Ser His Lys Leu Ser Ser Ala Arg  
210 215 220  
Thr Glu Ala His Ile Asn Ala Leu Lys Thr Val Thr Thr Phe Phe Cys  
225 230 235 240  
Phe Phe Val Ser Tyr Phe Ala Ala Phe Met Ala Asn Met Thr Phe Arg  
245 250 255  
Ile Pro Tyr Arg Ser His Gln Phe Phe Val Val Lys Glu Ile Met Ala  
260 265 270  
Ala Tyr Pro Ala Gly His Ser Val Ile Ile Val Leu Ser Asn Ser Lys  
275 280 285  
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290 295 300

<210> 25

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<212> PRT  
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<222> (2)  
<223> Phe or Gly

<220>  
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<222> (3)  
<223> Ile, Val or Leu

<220>  
<221> MOD\_RES  
<222> (4)  
<223> Val or Leu

<220>  
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<222> (6)  
<223> Ile or Val

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<223> Leu or Val

<220>  
<221> MOD\_RES  
<222> (10)  
<223> Gly or Thr

<220>  
<221> MOD\_RES  
<222> (13)  
<223> Val or Ala

<220>  
<221> MOD\_RES  
<222> (18)  
<223> Ile or Met

<220>  
<223> Description of Artificial Sequence: Consensus  
sequence

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Cys Xaa Asp Trp  
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<210> 26  
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<212> PRT  
<213> Artificial Sequence

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<223> Asp or Gly

<220>  
<221> MOD\_RES  
<222> (2)  
<223> Phe or Leu

<220>  
<221> MOD\_RES  
<222> (3)  
<223> Ile or Leu

<220>  
<221> MOD\_RES  
<222> (5)  
<223> Thr or Ile

<220>  
<221> MOD\_RES  
<222> (6)  
<223> Gly, Ala or Ser

<220>  
<221> MOD\_RES  
<222> (13)  
<223> Cys, Gly or Phe

<220>  
<223> Description of Artificial Sequence: Consensus sequence

<400> 26  
Xaa Xaa Xaa Leu Xaa Xaa Leu Ala Ile Ser Arg Ile Xaa Leu  
1 5 10

<210> 27  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> MOD\_RES  
<222> (3)  
<223> Leu or Phe

<220>  
<221> MOD\_RES  
<222> (4)  
<223> Ser, Thr or Asn

<220>  
<221> MOD\_RES  
<222> (5)  
<223> Leu, Ile or Val

<220>  
<221> MOD\_RES  
<222> (7)  
<223> Phe or Leu

<220>

&lt;221&gt; MOD\_RES

&lt;222&gt; (8)

&lt;223&gt; Ala or Thr

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (10)

&lt;223&gt; Cys, Ser or Asn

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (12)

&lt;223&gt; Ser, Asn or Gly

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (13)

&lt;223&gt; Ile or Val

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Consensus sequence

&lt;400&gt; 27

Asn His Xaa Xaa Xaa Trp Xaa Xaa Thr Xaa Leu Xaa Xaa  
1 5 10

&lt;210&gt; 28

&lt;211&gt; 18

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (3)

&lt;223&gt; Phe or Cys

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (8)

&lt;223&gt; Asn or Ser

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (11)

&lt;223&gt; His or Asn

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (12)

&lt;223&gt; Pro or Ser

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (13)

&lt;223&gt; Leu, Ile or Val

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (16)

&lt;223&gt; Trp or Tyr

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<220>  
<223> Description of Artificial Sequence: Consensus  
sequence

<400> 28  
Phe Tyr Xaa Leu Lys Ile Ala Xaa Phe Ser Xaa Xaa Xaa Phe Leu Xaa  
1 5 10 15  
Leu Lys

<210> 29  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> MOD\_RES  
<222> (4)  
<223> Ile, Phe or Val

<220>  
<221> MOD\_RES  
<222> (8)  
<223> Lys or Arg

<220>  
<221> MOD\_RES  
<222> (10)  
<223> Ser or Thr

<220>  
<221> MOD\_RES  
<222> (11)  
<223> Lys or Arg

<220>  
<221> MOD\_RES  
<222> (12)  
<223> Gln or Lys

<220>  
<221> MOD\_RES  
<222> (13)  
<223> Met or Ile

<220>  
<221> MOD\_RES  
<222> (14)  
<223> Gln or Lys

<220>  
<223> Description of Artificial Sequence: Consensus  
sequence

<400> 29  
Leu Leu Ile Xaa Ser Leu Trp Xaa His Xaa Xaa Xaa Xaa Xaa  
1 5 10

<210> 30  
<211> 14

<212> PRT  
<213> Artificial Sequence

<220>  
<221> MOD\_RES  
<222> (3)  
<223> Phe or Leu

<220>  
<221> MOD\_RES  
<222> (4)  
<223> Ile or Val

<220>  
<221> MOD\_RES  
<222> (7)  
<223> Leu or Met

<220>  
<221> MOD\_RES  
<222> (8)  
<223> Gly, Ser or Thr

<220>  
<221> MOD\_RES  
<222> (10)  
<223> Pro, Ser or Asn

<220>  
<221> MOD\_RES  
<222> (13)  
<223> Lys or Arg

<220>  
<221> MOD\_RES  
<222> (14)  
<223> Gln or Arg

<220>  
<223> Description of Artificial Sequence: Consensus  
sequence

<400> 30  
His Ser Xaa Xaa Leu Ile Xaa Xaa Asn Xaa Lys Leu Xaa Xaa  
1 5 10

<210> 31  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
peptide translocation domain

<400> 31  
Met Asn Gly Thr Glu Gly Pro Asn Phe Tyr Val Pro Phe Ser Asn Lys  
1 5 10 15  
Thr Gly Val Val  
20